



17

1/31

	1				50
EG327	MNKIYRIIWN	SALNAWVAVS	ELTRNHTKRA	SATVATAVLA	TLLFATVQAS.
BZ198	MNKIYRIIWN	SALNAWVVVS	ELTRNHTKRA	SATVATAVLA	TLLFATVQAN
BZ10	MNKISRIIWN	SALNAWVVVS	ELTRNHTKRA	SATVATAVLA	TLLFATVQAN
H15	MNKIYRIIWN	SALNAWVVVS	ELTRNHTKRA	SATVATAVLA	TLLFATVQAN
EG329	MNEILRIIWN	SALNAWVVVS	ELTRNHTKRA	SATVKTAVLA	TLLFATVQAS
PMC21	MNKIYRIIWN	SALNAWVVVS	ELTRNHTKRA	SATVKTAVLA	TLLFATVQAS
H38	MNKIYRIIWN	SALNAWVAVS	ELTRNHTKRA	SATVKTAVLA	TLLFATVQAN
P20	MNKIYRIIWN	SALNAWVVVS	ELTRNHTKRA	SATVATAVLA	TLLSATVQAN
Z2491	MNKIYRIIWN	SALNAWVAVS	ELTRNHTKRA	SATVKTAVLA	TLLFATVQAN
H41	MNKIYRIIWN	SALNAWVAVS	ELTRNHTKRA	SATVKTAVLA	TLLFATVQAN
Consensus	<u>MN-I-RIIWN</u>	<u>SALNAWV-VS</u>	<u>ELTRNHTKRA</u>	<u>SATV-TAVLA</u>	<u>TLL-ATVQA-</u>

C1

	51				100
EG327	TTDDD...DL	YLEPVQRTAV	VLSFRSDKEG	TGEKE.VTED	SNWGVYFDKK
BZ198	ATDDD...DL	YLEPVQRTAV	VLSFRSDKEG	TGEKE.GTED	SNWAVYFDEK
BZ10	ATDDD...DL	YLEPVQRTAV	VLSFRSDKEG	TGEKE.GTED	SNWAVYFDEK
H15	ATDDD...DL	YLEPVQRTAV	VLSFRSDKEG	TGEKE.GTED	SNWAVYFDEK
EG329	ANNEEQEEDL	YLDPVLRVA	VLIVNSDKEG	TGEKEKVEEN	SDWAVYFNEK
PMC21	ANNEEQEEDL	YLDPVQRTVA	VLIVNSDKEG	TGEKEKVEEN	SDWAVYFNEK
H38	ATDED...EEE	ELEPVRSAL	VLQFMIDKEG	NGENE.STGN	IGWSIYYDNH
P20	ATDTD...EDE	ELESVARSA	VLQFMIDKEG	NGEIESTGDI	GWSIYYDDHN
Z2491	ATDED...EEE	ELESVQR.SV	VGSIQASMEG	SGELET...I	SLSMTNDSKE
H41	ATDED...EEE	ELESVQR.SV	VGSIQASMEG	SVELET...I	SLSMTNDSKE
Consensus	-----	-L--V-R--	V-----EG	--E-E-----	-----

V1

	101				150
EG327	GVLTAGTITL	KAGDNLKIKQ	NTNENTNASS	....FTYSLK	KDLTDLTSVG
BZ198	RVLKAGAITL	KAGDNLKIKQ	NTNENTNDSS	....FTYSLK	KDLTDLTSVE
BZ10	RVLKAGAITL	KAGDNLKIKQ	NTNENTNENT	NDSSFTYSLK	KDLTDLTSVE
H15	RVLKAGAITL	KAGDNLKIKQ	NTNENTNENT	NDSSFTYSLK	KDLTDLTSVE
EG329	GVLTAIREITL	KAGDNLKIKQ	NG...TN...	....FTYSLK	KDLTDLTSVG
PMC21	GVLTAIREITL	KAGDNLKIKQ	NG...TN...	....FTYSLK	KDLTDLTSVG
H38	NTLHGATVTL	KAGDNLKIKQ	NTNKNTNENT	NDSSFTYSLK	KDLTDLTSVE
P20	TLHG.ATVTL	KAGDNLKIKQ	SGKD.....	....FTYSLK	KELKDLTSVE
Z2491	FVDPYIVVTL	KAGDNLKIKQ	NTNENTNASS	....FTYSLK	KDLTGGLINVE
H41	FVDPYIVVTL	KAGDNLKIKQ	NTNENTNASS	....FTYSLK	KDLTGGLINVE
Consensus	----- <u>TL</u>	<u>KAGDNLKIKQ</u>	-----	---- <u>FTYSLK</u>	<u>K-L--L--V-</u>

V1

C2

V2

C3

FIG. 1A



	151				200
EG327	TEKLSFSANS	NKVNITSDTK	GLNFAKKTAE	TNGDTTVHLN	GIGSTLTDTL
BZ198	TEKLSFGANG	NKVNITSDTK	GLNFAKETAG	TNGDPTVHLN	GIGSTLTDTL
BZ10	TEKLSFGANG	NKVNITSDTK	GLNFAKETAG	TNGDPTVHLN	GIGSTLTDTL
H15	TEKLSFGANG	NKVNITSDTK	GLNFAKETAG	TNGDPTVHLN	GIGSTLTDTL
EG329	TEKLSFSANG	NKVNITSDTK	GLNFAKETAG	TNGDTTVHLN	GIGSTLTDTL
PMC21	TEKLSFSANG	NKVNITSDTK	GLNFAKETAG	TNGDTTVHLN	GIGSTLTDTL
H38	TEKLSFGANG	NKVNITSDTK	GLNFAKETAG	TNGDPTVHLN	GIGSTLTDTL
P20	TEKLSFGANG	NKVNITSDTK	GLNFAKETAG	TNGDPTVHLN	GIGSTLTDTL
Z2491	TEKLSFGANG	KKVNIISDTK	GLNFAKETAG	TNGDPTVHLN	GIGSTLTDTL
H41	TEKLSFGANG	KKVNIISDTK	GLNFAKETAG	TNGDPTVHLN	GIGSTLTDM
Consensus	TEKLSF-AN-	-KVNI-SDTK	GLNFAK-TA-	TNGD-TVHLN	GIGSTLT-D-L
	C3				
	201				250
EG327	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN	AGWNIKGVP	GTTAS..DNV
BZ198	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN	AGWNIKGVP	GTTAS..DNV
BZ10	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN	AGWNIKGVP	GTTAS..DNV
H15	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN	AGWNIKGVP	GTTAS..DNV
EG329	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN	AGWNIKGVP	GTTAS..DNV
PMC21	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN	AGWNIKGVP	GTTAS..DNV
H38	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN	AGWNIKGVP	GTTAS..DNV
P20	AGSSASHVDA	GNQST..HYT	RAASIKDVLN	AGWNIKGVP	GSTTGQSENV
Z2491	AGSSASHVDA	GNQST..HYT	RAASIKDVLN	AGWNIKGVP	GSTTGQSENV
H41	LNTGATTNVT	NDNVTDDDEKK	RAASVKDVLN	AGWNIKGVP	GTTAS..DNV
Consensus	----A-----	----T-----	RAAS-KDVLN	AGWNIKGVP-	G-T-----NV
	V3		C4		V4
	251				300
EG327	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	RTEVKIGAKT	SVIKEKDGL
BZ198	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	RTEVKIGAKT	SVIKEKDGL
BZ10	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	RTEVKIGAKT	SVIKEKDGL
H15	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	RTEVKIGAKT	SVIKEKDGL
EG329	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	RTEVKIGAKT	SVIKEKDGL
PMC21	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	RTEVKIGAKT	SVIKEKDGL
H38	DFVHTYDTVE	FLSADTKTTT	VNVESKDNGK	RTEVKIGAKT	SVIKEKDGL
P20	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	RTEVKIGAKT	SVIKEKDGL
Z2491	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	RTEVKIGAKT	SVIKEKDGL
H41	DFVRTYDTVE	FLSADTKTTT	VNVESKDNGK	RTEVKIGAKT	SVIKEKDGL
Consensus	DFV-TYDTVE	FLSADTKTTT	VNVESKDNGK	-TEVKIGAKT	SVIKEKDGL
	C5				

FIG. 1B



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	301		350
EG327	VTGKDKGEND	SSTDKGEGLV	TAKEVIDAVN KAGWRMKTTT ANGQTGQADK
BZ198	VTGKGKDENG	SSTDGEGGLV	TAKEVIDAVN KAGWRMKTTT ANGQTGQADK
BZ10	VTGKGKGENG	SSTDGEGGLV	TAKEVIDAVN KAGWRMKTTT ANGQTGQADK
H15	VTGKGKDENG	SSTDGEGGLV	TAKEVIDAVN KAGWRMKTTT ANGQTGQADK
EG329	VTGKDKGEND	SSTDGEGGLV	TAKEVIDAVN KAGWRMKTTT ANGQTGQADK
PMC21	VTGKDKGEND	SSTDGEGGLV	TAKEVIDAVN KAGWRMKTTT ANGQTGQADK
H38	VTGKGKGENG	SSTDGEGGLV	TAKEVIDAVN KAGWRMKTTT ANGQTGQADK
P20	VTGKGKGENG	SSTDGEGGLV	TAKEVIDAVN KAGWRMKTTT ANGQTGQADK
Z2491	VTGKGKGENG	SSTDGEGGLV	TAKEVIDAVN KAGWRMKTTT ANGQTGQADK
H41	VTGKGKGENG	SSTDGEGGLV	TAKEVIDAVN KAGWRMKTTT ANGQTGQADK
Consensus	<u>VTGK-K-EN-</u>	<u>SSTD-GEGLV</u>	<u>TAKEVIDAVN KAGWRMKTTT ANGQTGQADK</u>

C5

	351		400
EG327	FETVTSGTNV	TFASGKGTTA	TVSKDDQGNI TVMYDVNVGD ALNVNQLQNS
BZ198	FETVTSGTNV	TFASGKGTTA	TVSKDDQGNI TVKYDVNVGD ALNVNQLQNS
BZ10	FETVTSGTKV	TFASGNGTTA	TVSKDDQGNI TVKYDVNVGD ALNVNQLQNS
H15	FETVTSGTKV	TFASGNGTTA	TVSKDDQGNI TVKYDVNVGD ALNVNQLQNS
EG329	FETVTSGTNV	TFASGKGTTA	TVSKDDQGNI TVMYDVNVGD ALNVNQLQNS
PMC21	FETVTSGTNV	TFASGKGTTA	TVSKDDQGNI TVMYDVNVGD ALNVNQLQNS
H38	FETVTSGTNV	TFASGKGTTA	TVSKDDQGNI TVKYDVNVGD ALNVNQLQNS
P20	FETVTSGTKV	TFASGNGTTA	TVSKDDQGNI TVKYDVNVGD ALNVNQLQNS
Z2491	FETVTSGTNV	TFASGKGTTA	TVSKDDQGNI TVMYDVNVGD ALNVNQLQNS
H41	FETVTSGTKV	TFASGNGTTA	TVSKDDQGNI TVKYDVNVGD ALNVNQLQNS
Consensus	<u>FETVTSGT-V</u>	<u>TFASG-GTTA</u>	<u>TVSKDDQGNI TV-YDVNVGD ALNVNQLQNS</u>

C5

	401		450
EG327	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EITRNGKNID
BZ198	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EITRNGKNID
BZ10	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EITRNGKNID
H15	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EITRNGKNID
EG329	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EITRNGKNID
PMC21	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EITRNGKNID
H38	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EITRNGKNID
P20	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EITRNGKNID
Z2491	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EISRNGKNID
H41	GWNLDSKAVA	GSSGKVISGN	VSPSKGKMDE TVNINAGNNI EITRNGKNID
Consensus	<u>GWNLDSKAVA</u>	<u>GSSGKVISGN</u>	<u>VSPSKGKMDE TVNINAGNNI EI-RNGKNID</u>

C5

FIG. 1C



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	451		500
EG327	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA LNVGSKDANK PVRITNVAPG
BZ198	IATSMAPQFS	SVSLGAGADA	PTLSVDDEGA LNVGSKDTNK PVRITNVAPG
BZ10	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA LNVGSKDANK PVRITNVAPG
H15	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA LNVGSKDANK PVRITNVAPG
EG329	IATSMTPQFS	SVSLGAGADA	PTLSVDG.DA LNVGSKKDNK PVRITNVAPG
PMC21	IATSMTPQFS	SVSLGAGADA	PTLSVDG.DA LNVGSKKDNK PVRITNVAPG
H38	IATSMTPQFS	SVSLGAGADA	PTLSVDDKGA LNVGSKDANK PVRITNVAPG
P20	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA LNVGSKDANK PVRITNVAPG
Z2491	IATSMAPQFS	SVSLGAGADA	PTLSVDDEGA LNVGSKDANK PVRITNVAPG
H41	IATSMTPQFS	SVSLGAGADA	PTLSVDDEGA LNVGSKDANK PVRITNVAPG
Consensus	<u>IATSM-PQFS</u>	<u>SVSLGAGADA</u>	<u>PTLSVD---A LNVGSK--NK PVRITNVAPG</u>

C5

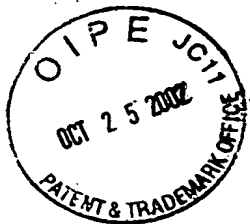
	501		550
EG327	VKEGDVTNVA	QLKGVAQNLN	NHIDNVDGNA RAGIAQAIAT AGLVQAYLPG
BZ198	VKEGDVTNVA	QLKGVAQNLN	NRIDNVDGNA RAGIAQAIAT AGLVQAYLPG
BZ10	VKEGDVTNVA	QLKGVAQNLN	NRIDNVDGNA RAGIAQAIAT AGLVQAYLPG
H15	VKEGDVTNVA	QLKGVAQNLN	NRIDNVDGNA RAGIAQAIAT AGLVQAYLPG
EG329	VKEGDVTNVA	QLKGVAQNLN	NRIDNVDGNA RAGIAQAIAT AGLVQAYLPG
PMC21	VKEGDVTNVA	QLKGVAQNLN	NRIDNVDGNA RAGIAQAIAT AGLVQAYLPG
H38	VKEGDVTNVA	QLKGVAQNLN	NRIDNVDGNA RAGIAQAIAT AGLVQAYLPG
P20	VKEGDVTNVA	QLKGVAQNLN	NRIDNVNGNA RAGIAQAIAT AGLVQAYLPG
Z2491	VKEGDVTNVA	QLKGVAQNLN	NRIDNVDGNA RAGIAQAIAT AGLVQAYLPG
H41	VKEGDVTNVA	QLKGVAQNLN	NRIDNVNGNA RAGIAQAIAT AGLVQAYLPG
Consensus	<u>VKEGDVTNVA</u>	<u>QLKGVAQNLN</u>	<u>N-IDNV-GNA RAGIAQAIAT AGL-QAYLPG</u>

C5

	551		600
EG327	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW IIKGTASGNS RGHFGASASV
BZ198	KSMMAIGGDT	YRGEAGYAIG	YSSISDGGNW IIKGTASGNS RGHFGASASV
BZ10	KSMMAIGGGT	YRGEAGYAIG	YSSISDTGNW VIKGTASGNS RGHFGTSASV
H15	KSMMAIGGGT	YRGEAGYAIG	YSSISDTGNW VIKGTASGNS RGHFGASASV
EG329	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW IIKGTASGNS RGHFGASASV
PMC21	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW IIKGTASGNS RGHFGASASV
H38	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW IIKGTASGNS RGHFGASASV
P20	KSMMAIGGGT	YLGEAGYAIG	YSSISDTGNW VIKGTASGNS RGHFGTSASV
Z2491	KSMMAIGGGT	YRGEAGYAIG	YSSISDGGNW IIKGTASGNS RGHFGASASV
H41	KSMMAIGGGT	YLGEAGYAIG	YSSISAGGNW IIKGTASGNS RGHFGASASV
Consensus	<u>KSMMAIGG-T</u>	<u>Y-GEAGYAIG</u>	<u>YSSIS--GNW -IKGTASGNS RGHFG-SASV</u>

C5

FIG. 1D



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	601
EG327	GYQW.
BZ198	GYQW.
BZ10	GYQW.
H15	GYQW.
EG329	GYQW.
PMC21	GYQW.
H38	GYQW.
P20	GYQW.
Z2491	GYQW.
H41	GYQW.
Consensus	<u>GYQW.</u>
	C5

**FIG. 1E**

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C1

C1

C1

V1

**FIG. 2A**



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	211								280
H15	GTGTTGAGCT	TCCGTTCCGA	TAAAGAAGGC	ACGGGAGAAA	AAGAAGGTAC	AGAAGA...T	TCAAATTGGG		
BZ10	GTGTTGAGCT	TCCGTTCCGA	TAAAGAAGGC	ACGGGAGAAA	AAGAAGGTAC	AGAAGA...T	TCAAATTGGG		
BZ198	GTGTTGAGCT	TCCGTTCCGA	TAAAGAAGGC	ACGGGAGAAA	AAGAAGGTAC	AGAAGA...T	TCAAATTGGG		
P20	GTGTTGCAAT	TCATGATCGA	TAAAGAAGGC	AATGGAGAAA	TCGAATCTAC	AGGAGA...T	ATAGGTTGGA		
H38	GTGTTGCAAT	TCATGATCGA	TAAAGAAGGC	AATGGAGAAA	ACGAATCTAC	AGGAAA...T	ATAGGTTGGA		
Z2491	GGG..AGCAT	TCAAG.CCAG	TATGGAAGGC	AGCGGCGAAT	TGGAAACGAT	ATCAT...T	ATCAATGACT		
H41	GTAGGGAGCA	TTCAAGCCAG	TATGGAAGGC	AGCGTCGAAT	TGGAAACGAT	A.....	TCATTATCAA		
EG329	GTGTTGATAG	TCAATTCCGA	TAAAGAAGGC	ACGGGAGAAA	AAGAAAAAGT	AGAAGAAAAT	TCAGATTGGG		
PMC21	GTGTTGATAG	TCAATTCCGA	TAAAGAAGGC	ACGGGAGAAA	AAGAAAAAGT	AGAAGAAAAT	TCAGATTGGG		
EG327	GTGTTGAGCT	TCCGTTCCGA	TAAAGAAGGC	ACGGGAGAAA	AAGAAGTTAC	AGAAGA...T	TCAAATTGGG		
Consensus	G-----	T-----C--	TA--GAAGGC	A--G--GAA-	--GAA-----	A-----	-----		

V1

	281								350
H15	CAGTATATTT	CGACGAGAAA	AGAGTACTAA	AAGCCGGAGC	AATCACCCTC	AAAGCCGGCG	ACAACCTGAA		
BZ10	CAGTATATTT	CGACGAGAAA	AGAGTACTAA	AAGCCGGAGC	AATCACCCTC	AAAGCCGGCG	ACAACCTGAA		
BZ198	CAGTATATTT	CGACGAGAAA	AGAGTACTAA	AAGCCGGAGC	AATCACCCTC	AAAGCCGGCG	ACAACCTGAA		
P20	GTATATATTA	CGACGATCAC	AACACTCTAC	ACGGCGCAAC	CGTTACCCTC	AAAGCCGGCG	ACAACCTGAA		
H38	GTATATATTA	CGACAATCAC	AACACTCTAC	ACGGCGCAAC	CGTTACCCTC	AAAGCCGGCG	ACAACCTGAA		
Z2491	AACGACAGCA	AGGAATTTGT	AGACCCATAC	ATAGTA....	.GTTACCCTC	AAAGCCGGCG	ACAACCTGAA		
H41	TGACTAACGA	CAGCAAGGAA	TTTGTAGACC	CATACATAGT	AGTTACCCTC	AAAGCCGGCG	ACAACCTGAA		
EG329	CAGTATATTT	CAACGAGAAA	GGAGTACTAA	CAGCCAGAGA	AATCACCCTC	AAAGCCGGCG	ACAACCTGAA		
PMC21	CAGTATATTT	CAACGAGAAA	GGAGTACTAA	CAGCCAGAGA	AATCACCCTC	AAAGCCGGCG	ACAACCTGAA		
EG327	GAGTATATTT	CGACAAGAAA	GGAGTACTAA	CAGCCGGAAC	AATCACCCTC	AAAGCCGGCG	ACAACCTGAA		
Consensus	-----A--	-----	-----	-----	--T-ACCCTC	AAAGCCGGCG	ACAACCTGAA		

V1

C2

	351								420
H15	AATCAAACAA	AACACCAATG	AAAACACCAA	TGAAAACACC	AATGACAGTA	GCTTCACCTA	CTCCCTGAAA		
BZ10	AATCAAACAA	AACACCAATG	AAAACACCAA	TGAAAACACC	AATGACAGTA	GCTTCACCTA	CTCCCTGAAA		
BZ198	AATCAAACAA	AACACCAATG	AAAACACC..	.....	AATGACAGTA	GCTTCACCTA	CTCCCTGAAA		
P20	AATCAAACAA	AGCGGCAAAG	A.....	.....	.....	.CTTCACCTA	CTCGCTGAAA		
H38	AATCAAACAA	AACACCAATA	AAAACACCAA	TGAAAACACC	AATGACAGTA	GCTTCACCTA	CTCGCTGAAA		
Z2491	AATCAAACAA	AACACCAATG	AAAACACC..	.....	AATGCCAGTA	GCTTCACCTA	CTCGCTGAAA		
H41	AATCAAACAA	AACACCAATG	AAAACACC..	.....	AATGCCAGTA	GCTTCACCTA	CTCGCTGAAA		
EG329	AATCAAACAA	AAC.....	.....G..	.....	....GCACAA	ACTTCACCTA	CTCGCTGAAA		
PMC21	AATCAAACAA	AAC.....	.....G..	.....	....GCACAA	ACTTCACCTA	CTCGCTGAAA		
EG327	AATCAAACAA	AACACCAATG	AAAACACC..	.....	AATGCCAGTA	GCTTCACCTA	CTCGCTGAAA		
Consensus	AATCAAACAA	A-C-----	-----	-----	-----	-CTTCACCTA	CTC-CTGAAA		

C2

V2

C3

FIG. 2B



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	421							490
H15	AAAGACCTCA	CAGATCTGAC	CAGTGTGAA	ACTGAAAAAT	TATCGTTTGG	CGCAAACGGT	AATAAAGTCA	
BZ10	AAAGACCTCA	CAGATCTGAC	CAGTGTGAA	ACTGAAAAAT	TATCGTTTGG	CGCAAACGGT	AATAAAGTCA	
BZ198	AAAGACCTCA	CAGATCTGAC	CAGTGTGAA	ACTGAAAAAT	TATCGTTTGG	CGCAAACGGT	AATAAAGTCA	
P20	AAAGAGCTGA	AAGACCTGAC	CAGTGTGAA	ACTGAAAAAT	TATCGTTTGG	CGCAAACGGT	AATAAAGTCA	
H38	AAAGACCTCA	CAGATCTGAC	CAGTGTGAA	ACTGAAAAAT	TATCGTTTGG	CGCAAACGGC	AATAAAGTCA	
Z2491	AAAGACCTCA	CAGGCCTGAT	CAATGTTGAA	ACTGAAAAAT	TATCGTTTGG	CGCAAACGGC	AAGAAAGTCA	
H41	AAAGACCTCA	CAGGCCTGAT	CAATGTTGAA	ACTGAAAAAT	TATCGTTTGG	CGCAAACGGC	AAGAAAGTCA	
EG329	AAAGACCTCA	CAGATCTGAC	CAGTGTGGA	ACTGAAAAAT	TATCGTTTAG	CGCAAACGGC	AATAAAGTCA	
PMC21	AAAGACCTCA	CAGATCTGAC	CAGTGTGGA	ACTGAAAAAT	TATCGTTTAG	CGCAAACGGC	AATAAAGTCA	
EG327	AAAGACCTCA	CAGATCTGAC	CAGTGTGGA	ACTGAAAAAT	TATCGTTTAG	CGCAAACAGC	AATAAAGTCA	
Consensus	AAAGA-CT-A	-AG--CTGA-	CA-TGTTG-A	ACTGAAAAAT	TATCGTTT-G	CGCAAAC-G-	AA-AAAGTCA	

C3

	491							560
H15	ACATCACAAAG	CGACACCAAA	GGCTTGAATT	TTGCGAAAGA	AACGGCTGGG	ACGAACGGCG	ACCCCACGGT	
BZ10	ACATCACAAAG	CGACACCAAA	GGCTTGAATT	TTGCGAAAGA	AACGGCTGGG	ACGAACGGCG	ACCCCACGGT	
BZ198	ACATCACAAAG	CGACACCAAA	GGCTTGAATT	TTGCGAAAGA	AACGGCTGGG	ACGAACGGCG	ACCCCACGGT	
P20	ACATCACAAAG	CGACACCAAA	GGCTTGAATT	TTGCGAAAGA	AACGGCTGGG	ACGAACGGCG	ACCCCACGGT	
H38	ACATCACAAAG	CGACACCAAA	GGCTTGAATT	TCGCGAAAGA	AACGGCTGGG	ACGAACGGCG	ACACCACGGT	
Z2491	ACATCATAAG	CGACACCAAA	GGCTTGAATT	TCGCGAAAGA	AACGGCTGGG	ACGAACGGCG	ACACCACGGT	
H41	ACATCATAAG	CGACACCAAA	GGCTTGAATT	TCGCGAAAGA	AACGGCTGGG	ACGAACGGCG	ACACCACGGT	
EG329	ACATCACAAAG	CGACACCAAA	GGCTTGAATT	TTGCGAAAGA	AACGGCTGGG	ACGAACGGCG	ACACCACGGT	
PMC21	ACATCACAAAG	CGACACCAAA	GGCTTGAATT	TTGCGAAAGA	AACGGCTGGG	ACGAACGGCG	ACACCACGGT	
EG327	ACATCACAAAG	CGACACCAAA	GGCTTGAATT	TCGCGAAAAA	AACGGCTGAG	ACCAACGGCG	ACACCACGGT	
Consensus	ACATCA-AAG	CGACACCAAA	GGCTTGAATT	T-GCGAAA-A	AACGGCTG-G	AC-AACGGCG	AC-CCACGGT	

C3

	561							630
H15	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC	CGATACGCTG	CTGAATACCG	GAGCGACCAC	AAACGTAACC	
BZ10	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC	CGATACGCTG	CTGAATACCG	GAGCGACCAC	AAACGTAACC	
BZ198	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC	CGATACGCTG	CTGAATACCG	GAGCGACCAC	AAACGTAACC	
P20	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC	CGATACGCTT	GCGGGTTCTT	CTGCTTCTCA	CGTTGATGCG	
H38	TCATCTGAAC	GGTATTGGTT	CGACTTTGAC	CGATACGCTG	CTGAATACCG	GAGCGACCAC	AAACGTAACC	
Z2491	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC	CGATACGCTT	GCGGGTTCTT	CTGCTTCTCA	CGTTGATGCG	
H41	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC	CGATATGCTG	CTGAATACCG	GAGCGACCAC	AAACGTAACC	
EG329	TCATCTGAAC	GGTATTGGTT	CGACTTTGAC	CGATACGCTG	CTGAATACCG	GAGCGACCAC	AAACGTAACC	
PMC21	TCATCTGAAC	GGTATTGGTT	CGACTTTGAC	CGATACGCTG	CTGAATACCG	GAGCGACCAC	AAACGTAACC	
EG327	TCATCTGAAC	GGTATCGGTT	CGACTTTGAC	CGATACGCTG	CTGAATACCG	GAGCGACCAC	AAACGTAACC	
Consensus	TCATCTGAAC	GGTAT-GGTT	CGACTTTGAC	CGATA-GCT-	--G--T-C--	--GC--C--	----G--C-	

C3

V3

FIG.2C





9/31

631 700

H15	AACGACAACG	TTACCGATGA	CGAGAAAAAA	CGTGCGGCAA	GC GTTAAAGA	CGTATTAAAC	GCAGGCTGGA
BZ10	AACGACAACG	TTACCGATGA	CGAGAAAAAA	CGTGCGGCAA	GC GTTAAAGA	CGTATTAAAC	GCAGGCTGGA
BZ198	AACGACAACG	TTACCGATGA	CGAGAAAAAA	CGTGCGGCAA	GC GTTAAAGA	CGTATTAAAC	GCAGGCTGGA
P20	GGTAACCAAA	GTACACATTA	C.....ACT	CGTGCAAGCA	GTATTAAAGG	TGTGTTGAAT	GCAGGCTGGA
H38	AACGACAACG	TTACCGATGA	CAAGAAAAAA	CGTGCGGCAA	GC GTTAAAGA	CGTATTAAAC	GCAGGCTGGA
Z2491	GGTAACCAAA	GTACACATTA	C.....ACT	CGTGCAAGCA	GTATTAAAGG	TGTGTTGAAT	GCAGGCTGGA
H41	AACGACAACG	TTACCGATGA	CGAGAAAAAA	CGTGCGGCAA	GC GTTAAAGA	CGTATTAAAC	GCAGGCTGGA
EG329	AACGACAACG	TTACCGATGA	CGAGAAAAAA	CGTGCGGCAA	GC GTTAAAGA	CGTATTAAAC	GCAGGCTGGA
PMC21	AACGACAACG	TTACCGATGA	CGAGAAAAAA	CGTGCGGCAA	GC GTTAAAGA	CGTATTAAAC	GCAGGCTGGA
EG327	AACGACAACG	TTACCGATGA	CGAGAAAAAA	CGTGCGGCAA	GC GTTAAAGA	CGTATTAAAC	GCAGGCTGGA
Consensus	----AC-A--	-TAC--AT-A	C-----A--	CGTGC-GCAA	G--TTAA-GA	-GT-TT-AA-	GC-GG-TGGA

V3 C4

701 770

H15	ACATTAAAGG	CGTTAAACCC	GGTACAACAG	CT.....TC	CGATAACGTT	GATTTCGTCC	GCACTTACGA
BZ10	ACATTAAAGG	CGTTAAACCC	GGTACAACAG	CT.....TC	CGATAACGTC	GATTTCGTCC	GCACTTACGA
BZ198	ACATTAAAGG	CGTTAAACCC	GGTACAACAG	CT.....TC	CGATAACGTT	GATTTCGTCC	GCACTTACGA
P20	ATATTAAAGG	TGTTAAACT	GGCTCAACAA	CTGGTCAATC	AGAAAATGTC	GATTTCGTCC	GCACTTACGA
H38	ACATTAAAGG	CGTTAAACCC	GGTACAACAG	CT.....TC	CGATAACGTT	GATTTCGTCC	GCACTTACGA
Z2491	ATATTAAAGG	TGTTAAACT	GGCTCAACAA	CTGGTCAATC	AGAAAATGTC	GATTTCGTCC	GCACTTACGA
H41	ACATTAAAGG	CGTTAAACCC	GGTACAACAG	CT.....TC	CGATAACGTT	GATTTCGTCC	GCACTTACGA
EG329	ACATTAAAGG	CGTTAAACCC	GGTACAACAG	CT.....TC	CGATAACGTT	GATTTCGTCC	GCACTTACGA
PMC21	ACATTAAAGG	CGTTAAACCC	GGTACAACAG	CT.....TC	CGATAACGTT	GATTTCGTCC	GCACTTACGA
EG327	ACATTAAAGG	CGTTAAACCC	GGTACAACAG	CT.....TC	CGATAACGTT	GATTTCGTCC	GCACTTACGA
Consensus	A-ATTAA-GG	-GTTAA-C-	GG--CAACA-	CT-----TC	-GA-AA-GT-	GATTTCGTCC	-CACTTACGA

C4 V4 C5

771 840

H15	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
BZ10	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
BZ198	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
P20	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
H38	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
Z2491	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
H41	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
EG329	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
PMC21	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
EG327	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG
Consensus	CACAGTCGAG	TTCTTGAGCG	CAGATACGAA	AACAACGACT	GTTAATGTGG	AAAGCAAAGA	CAACGGCAAG

C5

841 910

H15	AAAACCGAAG	TTAAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
BZ10	AGAACCGAAG	TTAAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
BZ198	AAAACCGAAG	TTAAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
P20	AGAACCGAAG	TTAAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
H38	AGAACCGAAG	TTAAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
Z2491	AGAACCGAAG	TTAAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
H41	AAAACCGAAG	TTAAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
EG329	AAAACCGAAG	TTAAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
PMC21	AAAACCGAAG	TTAAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
EG327	AGAACCGAAG	TTAAAATCGG	TGCGAAGACT	TCTGTTATTA	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA
Consensus	A-AACCGAAG	TTAAAATCGG	TGCGAAGACT	TCTGTTAT-A	AAGAAAAAGA	CGGTAAGTTG	GTTACTGGTA

C5

FIG. 2D



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911 980  
H15 AAGGCAAAGA CGAGAATGGT TCTTCTACAG ACGAAGGCCA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA  
B210 AAGGCAAAGG CGAGAATGGT TCTTCTACAG ACGAAGGCCA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA  
BZ198 AAGGCAAAGA CGAGAATGGT TCTTCTACAG ACGAAGGCCA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA  
P20 AAGGCAAAGG CGAGAATGGT TCTTCTACAG ACGAAGGCCA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA  
H38 AAGGCAAAGG CGAGAATGGT TCTTCTACAG ACGAAGGCCA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA  
Z2491 AAGGCAAAGG CGAGAATGGT TCTTCTACAG ACGAAGGCCA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA  
H41 AAGGCAAAGG CGAGAATGGT TCTTCTACAG ACGAAGGCCA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA  
EG329 AAGACAAAGG CGAGAATGGT TCTTCTACAG ACGAAGGCCA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA  
PMC21 AAGACAAAGG CGAGAATGGT TCTTCTACAG ACGAAGGCCA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA  
EG327 AAGACAAAGG CGAGAATGAT TCTTCTACAG ACGAAGGCCA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA  
Consensus AAG-CAAAG- CGAGAATG-T TCTTCTACAG AC-AAGGCCA AGGCTTAGTG ACTGCAAAAG AAGTGATTGA

C5

981 1050  
H15 TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG  
B210 TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG  
BZ198 TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG  
P20 TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG  
H38 TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG  
Z2491 TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG  
H41 TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG  
EG329 TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG  
PMC21 TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG  
EG327 TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG  
Consensus TGCAGTAAAC AAGGCTGGTT GGAGAATGAA AACAACAACC GCTAATGGTC AAACAGGTCA AGCTGACAAG

C5

1051 1120  
H15 TTTGAAACCG TTACATCAGG CACAAAAGTA ACCTTTGCTA GTGGTAATGG TACAACGCG ACTGTAAGTA  
B210 TTTGAAACCG TTACATCAGG CACAAAAGTA ACCTTTGCTA GTGGTAATGG TACAACGCG ACTGTAAGTA  
BZ198 TTTGAAACCG TTACATCAGG CACAAAAGTA ACCTTTGCTA GTGGTAATGG TACAACGCG ACTGTAAGTA  
P20 TTTGAAACCG TTACATCAGG CACAAAAGTA ACCTTTGCTA GTGGTAATGG TACAACGCG ACTGTAAGTA  
H38 TTTGAAACCG TTACATCAGG CACAAAAGTA ACCTTTGCTA GTGGTAATGG TACAACGCG ACTGTAAGTA  
Z2491 TTTGAAACCG TTACATCAGG CACAAAAGTA ACCTTTGCTA GTGGTAATGG TACAACGCG ACTGTAAGTA  
H41 TTTGAAACCG TTACATCAGG CACAAAAGTA ACCTTTGCTA GTGGTAATGG TACAACGCG ACTGTAAGTA  
EG329 TTTGAAACCG TTACATCAGG CACAAAAGTA ACCTTTGCTA GTGGTAATGG TACAACGCG ACTGTAAGTA  
PMC21 TTTGAAACCG TTACATCAGG CACAAAAGTA ACCTTTGCTA GTGGTAATGG TACAACGCG ACTGTAAGTA  
EG327 TTTGAAACCG TTACATCAGG CACAAAAGTA ACCTTTGCTA GTGGTAATGG TACAACGCG ACTGTAAGTA  
Consensus TTTGAAACCG TTACATCAGG CACAAA-GTA ACCTTTGCTA GTGGTAA-GG TACAACGCG ACTGTAAGTA

C5

1121 1190  
H15 AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGTAAA TGTCGGCGAT GCCCTAAACG TCAATCAGCT  
B210 AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGTAAA TGTCGGCGAT GCCCTAAACG TCAATCAGCT  
BZ198 AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGTAAA TGTCGGCGAT GCCCTAAACG TCAATCAGCT  
P20 AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGTAAA TGTCGGCGAT GCCCTAAACG TCAATCAGCT  
H38 AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGTAAA TGTCGGCGAT GCCCTAAACG TCAATCAGCT  
Z2491 AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGTAAA TGTCGGCGAT GCCCTAAACG TCAATCAGCT  
H41 AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGTAAA TGTCGGCGAT GCCCTAAACG TCAATCAGCT  
EG329 AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGTAAA TGTCGGCGAT GCCCTAAACG TCAATCAGCT  
PMC21 AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGTAAA TGTCGGCGAT GCCCTAAACG TCAATCAGCT  
EG327 AAGATGATCA AGGCAACATC ACTGTTAAGT ATGATGTAAA TGTCGGCGAT GCCCTAAACG TCAATCAGCT  
Consensus AAGATGATCA AGGCAACATC ACTGTTA-GT ATGATGTAAA TGTCGGCGAT GCCCTAAACG TCAATCAGCT

C5

FIG. 2E



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1191 1260  
H15 GCAAAACAGC GGTGGGAATT TGGATTCCAA AGCGGTTGCA GGTCTTCGG GCAAAGTCAT CAGCGGCAAT  
B210 GCAAAACAGC GGTGGGAATT TGGATTCCAA AGCGGTTGCA GGTCTTCGG GCAAAGTCAT CAGCGGCAAT  
B2198 GCAAAACAGC GGTGGGAATT TGGATTCCAA AGCGGTTGCA GGTCTTCGG GCAAAGTCAT CAGCGGCAAT  
P20 GCAAAACAGC GGTGGGAATT TGGATTCCAA AGCGGTTGCA GGTCTTCGG GCAAAGTCAT CAGCGGCAAT  
H38 GCAAAACAGC GGTGGGAATT TGGATTCCAA AGCGGTTGCA GGTCTTCGG GCAAAGTCAT CAGCGGCAAT  
Z2491 GCAAAACAGC GGTGGGAATT TGGATTCCAA AGCGGTTGCA GGTCTTCGG GCAAAGTCAT CAGCGGCAAT  
H41 GCAAAACAGC GGTGGGAATT TGGATTCCAA AGCGGTTGCA GGTCTTCGG GCAAAGTCAT CAGCGGCAAT  
EG329 GCAAAACAGC GGTGGGAATT TGGATTCCAA AGCGGTTGCA GGTCTTCGG GCAAAGTCAT CAGCGGCAAT  
PMC21 GCAAAACAGC GGTGGGAATT TGGATTCCAA AGCGGTTGCA GGTCTTCGG GCAAAGTCAT CAGCGGCAAT  
EG327 GCAAAACAGC GGTGGGAATT TGGATTCCAA AGCGGTTGCA GGTCTTCGG GCAAAGTCAT CAGCGGCAAT  
Consensus GCAAAACAGC GGTGGGAATT TGGATTCCAA AGCGGTTGCA GGTCTTCGG GCAAAGTCAT CAGCGGCAAT

C5

1261 1330  
H15 GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC  
B210 GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC  
B2198 GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC  
P20 GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC  
H38 GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC  
Z2491 GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC  
H41 GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC  
EG329 GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC  
PMC21 GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC  
EG327 GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC  
Consensus GTTTCGCCGA GCAAGGGAAA GATGGATGAA ACCGTCAACA TTAATGCCGG CAACAACATC GAGATTACCC

C5

1331 1400  
H15 GCAACGGCAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG  
B210 GCAACGGCAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG  
B2198 GCAACGGTAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG  
P20 GCAACGGTAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG  
H38 GCAACGGTAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG  
Z2491 GCAACGGTAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG  
H41 GCAACGGCAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG  
EG329 GCAACGGTAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG  
PMC21 GCAACGGTAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG  
EG327 GCAACGGCAA AAATATCGAC ATCGCCACTT CGATGACCCC GCAATTTTCC AGCGTTTCGC TCGGCGCGGG  
Consensus GCAACGG-AA AAATATCGAC ATCGCCACTT CGATG-C-CC GCA-TTTTCC AGCGTTTCGC TCGG-GCGGG

C5

1401 1470  
H15 GGCGGATGCG CCCACTTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTCG GCAGCAAGGA TGCCAACAAA  
B210 GGCGGATGCG CCCACTTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTCG GCAGCAAGGA TGCCAACAAA  
B2198 GGCGGATGCG CCCACTTTGA GCGTGGATGA CGAGGGCGCG TTGAATGTCG GCAGCAAGGA TACCAACAAA  
P20 GGCGGATGCG CCCACTTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTCG GCAGCAAGGA TGCCAACAAA  
H38 GGCGGATGCG CCCACTTTGA GCGTGGATGA CAAGGGCGCG TTGAATGTCG GCAGCAAGGA TGCCAACAAA  
Z2491 GGCAGATGCG CCCACTTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTCG GCAGCAAGGA TGCCAACAAA  
H41 GGCGGATGCG CCCACTTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTCG GCAGCAAGGA TGCCAACAAA  
EG329 GGCGGATGCG CCCACTTTGA GCGTGGAT.. .GGGGACGCA TTGAATGTCG GCAGCAAGGA GGACAACAAA  
PMC21 GGCGGATGCG CCCACTTTGA GCGTGGAT.. .GGGGACGCA TTGAATGTCG GCAGCAAGGA GGACAACAAA  
EG327 GGCGGATGCG CCCACTTTAA GCGTGGATGA CGAGGGCGCG TTGAATGTCG GCAGCAAGGA TGCCAACAAA  
Consensus GGC-GATGCG CCCACTTT-A GCGTGGAT-- --GG-CG- TTGAATGTCG GCAGCAAG-A ---CAACAAA

C5

FIG. 2F



12/31

1471 1540  
H15 CCCGTCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG  
BZ10 CCCGTCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG  
BZ198 CCCGTCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG  
P20 CCCGTCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG  
H38 CCCGTCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG  
Z2491 CCCGTCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG  
H41 CCCGTCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG  
EG329 CCCGTCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG  
PMC21 CCCGTCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG  
EG327 CCCGTCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG  
Consensus CCCGTCGCA TTACCAATGT CGCCCCGGGC GTTAAAGAGG GGGATGTTAC AAACGTCGCA CAACTTAAAG

C5

1541 1610  
H15 GTGTGGCGCA AAAC TTGAAC AACC GCATCG ACAATGTGGA CGGCAACGCG CGCGCGGGTA TCGCCCAAGC  
BZ10 GTGTGGCGCA AAAC TTGAAC AACC GCATCG ACAATGTGGA CGGCAACGCG CGCGCGGGTA TCGCCCAAGC  
BZ198 GCGTGGCGCA AAAC TTGAAC AACC GCATCG ACAATGTGGA CGGCAACGCG CGCGCGGGTA TCGCCCAAGC  
P20 GTGTGGCGCA AAAC TTGAAC AACC GCATCG ACAATGTGGA CGGCAACGCG CGCGCGGGTA TCGCCCAAGC  
H38 GCGTGGCGCA AAAC TTGAAC AACC GCATCG ACAATGTGGA CGGCAACGCG CGTGCGGGCA TCGCCCAAGC  
Z2491 GCGTGGCGCA AAAC TTGAAC AACC GCATCG ACAATGTGGA CGGCAACGCG CGTGCGGGCA TCGCCCAAGC  
H41 GTGTGGCGCA AAAC TTGAAC AACC GCATCG ACAATGTGGA CGGCAACGCG CGTGCGGGCA TCGCCCAAGC  
EG329 GCGTGGCGCA AAAC TTGAAC AACC GCATCG ACAATGTGGA CGGCAACGCG CGTGCGGGCA TCGCCCAAGC  
PMC21 GCGTGGCGCA AAAC TTGAAC AACC GCATCG ACAATGTGGA CGGCAACGCG CGTGCGGGCA TCGCCCAAGC  
EG327 GCGTGGCGCA AAAC TTGAAC AACC GCATCG ACAATGTGGA CGGCAACGCG CGTGCGGGCA TCGCCCAAGC  
Consensus G-GTGGCGCA AAAC TTGAAC AACC-CATCG ACAATGTG-A CGGCAACGCG CG-GCGGG-A TCGCCCAAGC

C5

1611 1680  
H15 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTA  
BZ10 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTA  
BZ198 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTA  
P20 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTA  
H38 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTA  
Z2491 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTA  
H41 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTA  
EG329 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTA  
PMC21 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTA  
EG327 GATTGCAACC GCAGGTTTGG CTCAGGCGTA TTTGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTA  
Consensus GATTGCAACC GCAGGTTTGG -TCAGGCGTA T-TGCCCGGC AAGAGTATGA TGGCGATCGG CGGCGGTA

C5

FIG. 2G

[illegible]

	1751				1815
H15	GCACGGCTTC	CGGCAATTGG	CGCGGCCAATT	TCGGTGCCTTC	CGCATCTGTC
BZ10	GCACGGGTTT	CGGCAAAATCG	CGCGGTCAATT	TCGGTGACTTC	CGCATCTGTC
BZ198	GCACGGGTTT	CGGCAAAATCG	CGCGGCCAATT	TCGGTGCTTTC	CGCATCTGTC
P20	GCACGGGTTT	CGGCAAAATCG	CGCGGTCAATT	TCGGTGCTTTC	CGCATCTGTC
H38	GCACGGGTTT	CGGCAAAATCG	CGCGGTCAATT	TCGGTGCTTTC	CGCATCTGTC
Z2491	GCACGGGTTT	CGGCAAAATCG	CGCGGCCAATT	TCGGTGCTTTC	CGCATCTGTC
H41	GCACGGGTTT	CGGCAAAATCG	CGCGGCCAATT	TCGGTGCTTTC	CGCATCTGTC
EG329	GCACGGGTTT	CGGCAAAATCG	CGCGGCCAATT	TCGGTGCTTTC	CGCATCTGTC
PMC21	GCACGGGTTT	CGGCAAAATCG	CGCGGCCAATT	TCGGTGCTTTC	CGCATCTGTC
EG327	GCACGGGTTT	CGGCAAAATCG	CGCGGCCAATT	TCGGTGCTTTC	CGCATCTGTC
Consensus	<u>GCACGGGCTTC</u>	<u>CGGCAAAATCG</u>	<u>CGCGG-CATT</u>	<u>TCGGT-CTTC</u>	<u>CGCATCTGTC</u>
				C5	
					GGTATCA-T
					GGTAA

**FIG. 2H**



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1 50  
H41 MNKIYRIIWN SALNAWVAVS ELTRNHTKRA SATVKTAVLA TLLFATVOAN  
PMC21 MNKIYRIIWN SALNAWVVVS DLTRNHTKRA SATVNTAVLA TLLFATVOAS  
H41Studel MNKIYRIIWN SALNAWVAVS ELTRNHTKRA SATVKTAVLA TLLFATVOAN  
PMC21Bglde1 MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVOAS  
PMC21C1C5 MNKIYRIIWN SALNAWVVVS ELTRNHTKRA SATVKTAVLA TLLFATVOAS

C1

51 100  
H41 ATDED...EEE ELESVQRS.V VGSIQASMEG SVELET...I SLSMTNDSKE  
PMC21 ANNEEQEEYL YLHPVQRTVA VLIVNSDKEG AGEKEKVEEN SDWAVYFNEK  
H41Studel ATDE.....  
PMC21Bglde1 ANNE.....  
PMC21C1C5 AN.....

V1

101 150  
H41 FVDPYIVVTI KAGDNLKIKO N.TNENTNAS SFTYSLKKDL TGLINVETEK  
PMC21 GVLTAIREITL KAGDNLKIKO NGTN.....FTYSLKKDL TDLTSVGTEK  
H41Studel ..... TGLINVETEK  
PMC21Bglde1 ..... TDLTSVGTEK  
PMC21C1C5 .....

V1 C2 V2 C3

151 200  
H41 LSFGANGKKV NIISDTKGLN FAKETAGTNG DTTVHLNGIG STLTDMLLNT  
PMC21 LSFSAHGKLV NIISDTKGLN FAKETAGTNG DTTVHLNGIG STLTDLTLNT  
H41Studel LSFGANGKKV NIISDTKGLN FAKETAGTNG DTTVHLNGIG STLTDMLLNT  
PMC21Bglde1 LSFSAHGKLV NIISDTKGLN FAKETAGTNG DTTVHLNGIG STLTDLTLNT  
PMC21C1C5 .....

C3

V3

201 250  
H41 GATTNVTNDN VTDDEKKRAA SVKDVLNAGW NIKGVKPGTT ASDNVDFVRT  
PMC21 GATTNVTNDN VTDDEKKRAA SVKDVLNAGW NIKGVKPGTT ASDNVDFVRT  
H41Studel GATTNVTNDN VTDDEKKRAA SVKDVLNAGW NIKGVKPGTT ASDNVDFVRT  
PMC21Bglde1 GATTNVTNDN VTDDEKKRAA SVKDVLNAGW NIKGVKPGTT ASDNVDFVRT  
PMC21C1C5 .....NVDFVRT

V3

C4

V4

C5

251 300  
H41 YDTVEFLSAD TKTTTVNVES KDNGKKTEVK IGAKTSVIKE KDGKLVGTGK  
PMC21 YDTVEFLSAD TKTTTVNVES KDNGKKTEVK IGAKTSVIKE KDGKLVGTGD  
H41Studel YDTVEFLSAD TKTTTVNVES KDNGKKTEVK IGAKTSVIKE KDGKLVGTGK  
PMC21Bglde1 YDTVEFLSAD TKTTTVNVES KDNGKKTEVK IGAKTSVIKE KDGKLVGTGD  
PMC21C1C5 YDTVEFLSAD TKTTTVNVES KDNGKKTEVK IGAKTSVIKE KDGKLVGTGD

C5

301 350  
H41 KGENGSSTDE GEGLVTAKEV IDAVNKAGWR MKTTTANGQT GOADKFETVT  
PMC21 KGENGSSTDE GEGLVTAKEV IDAVNKAGWR MKTTTANGQT GOADKFETVT  
H41Studel KGENGSSTDE GEGLVTAKEV IDAVNKAGWR MKTTTANGQT GOADKFETVT  
PMC21Bglde1 KGENGSSTDE GEGLVTAKEV IDAVNKAGWR MKTTTANGQT GOADKFETVT  
PMC21C1C5 KGENGSSTDE GEGLVTAKEV IDAVNKAGWR MKTTTANGQT GOADKFETVT

C5

351 400  
H41 SGTKVTFASG NGTTATVSKD DOGNITVKYD VNVGDALNVN QLQNSGWNLD  
PMC21 SGTNVTFASG KGTTATVSKD DOGNITVMYD VNVGDALNVN QLQNSGWNLD  
H41Studel SGTKVTFASG NGTTATVSKD DOGNITVKYD VNVGDALNVN QLQNSGWNLD  
PMC21Bglde1 SGTNVTFASG KGTTATVSKD DOGNITVMYD VNVGDALNVN QLQNSGWNLD  
PMC21C1C5 SGTNVTFASG KGTTATVSKD DOGNITVMYD VNVGDALNVN QLQNSGWNLD

C5

FIG. 10A



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401 450  
H41 SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM  
PMC21 SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM  
H41Studel SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM  
PMC21Bgldel SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM  
PMC21C1C5 SKAVAGSSGK VISGNVSPSK GKMDETVNIN AGNNIEITRN GKNIDIATSM  
C5

451 500  
H41 TPOFSSVSLG AGADAPTLV DDEGALNVGS KDANKPVVIT NVAPGVKEGD  
PMC21 TPOFSSVSLG AGADAPTLV DG.DALNVGS KKDANKPVVIT NVAPGVKEGD  
H41Studel TPOFSSVSLG AGADAPTLV DDEGALNVGS KDANKPVVIT NVAPGVKEGD  
PMC21Bgldel TPOFSSVSLG AGADAPTLV DG.DALNVGS KKDANKPVVIT NVAPGVKEGD  
PMC21C1C5 TPOFSSVSLG AGADAPTLV DG.DALNVGS KKDANKPVVIT NVAPGVKEGD  
C5

501 550  
H41 VTNVAQLKGV AQNLNNRIDN VNGNARAGIA QAIATAGLVQ AYLPGKSMMMA  
PMC21 VTNVAQLKGV AQNLNNRIDN VDG NARAGIA QAIATAGLVQ AYLPGKSMMMA  
H41Studel VTNVAQLKGV AQNLNNRIDN VNGNARAGIA QAIATAGLVQ AYLPGKSMMMA  
PMC21Bgldel VTNVAQLKGV AQNLNNRIDN VDG NARAGIA QAIATAGLVQ AYLPGKSMMMA  
PMC21C1C5 VTNVAQLKGV AQNLNNRIDN VDG NARAGIA QAIATAGLVQ AYLPGKSMMMA  
C5

551 600  
H41 IGGGTYLGEA GYAIGYSSIS AGGNWIIKGT ASGNSRGHFG ASASVGYOW.  
PMC21 IGGGTYRGEA GYAIGYSSIS DGGNWIIGT ASGNSRGHFG ASASVGYOW.  
H41Studel IGGGTYLGEA GYAIGYSSIS AGGNWIIKGT ASGNSRGHFG ASASVGYOW.  
PMC21Bgldel IGGGTYRGEA GYAIGYSSIS DGGNWIIGT ASGNSRGHFG ASASVGYOW.  
PMC21C1C5 IGGGTYRGEA GYAIGYSSIS DGGNWIIGT ASGNSRGHFG ASASVGYOW.  
C5

FIG. 10B